

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC
TGTGCCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGGC
GTTTGGCCCAGGACGGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTTGCTGGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT
CTGAGGACCGGGAGACAGCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCTGCT
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTGCT
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGCAAAGACCAAGATATTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS
SRKQQNVVDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLTDINVKAPALMTKAVVPEMEKRGGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCCGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCAGGCGGCG
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCTGCAGAACCAGGTGGC
GCGGCTGGAGGAGGAGAACCAGAGACTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAACTGC
AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGCGG
CCAGGCTGGGGGGGCTGCGGCTCCTGAATGGCCTGCCTCCCGGGTCTTTGTGCCTCGACCTCATAC
AGCCCCCTGGGGGGTGGCCACGCCCATGTGCTGGGCATGGTGCCGCTGCCTGCCTCCCTGGAGATG
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGCCGCC
CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCACGCCCAG
GGAGTCTGCCAGAGAGGAAGGGCCCAGAGCTTTGCCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC
AGAGCAGTTGGTGGGAGCAAGGCCCGAGTTAGGCCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG
GCGGCTGGCCCAGGCCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA
TTGGCGAGCTGGTCCGCACAGGAAAGGCAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGCAGGAGGGTCTGCTG
CGCCCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTACTGTGCTG
GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGAGGGACA
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA
GAGATCGCGGCTTCCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAGCCTGGAACAGCA
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA
GCGCCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGTGCTC
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCGAGGAGGAGCGGAC
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA
CATGCCGCCAGCGGGTGCTTCGGGCCCTCAGCCTCGTTGCTGTCCAGTGCGAGATGAACCTCATGGCC
AAGCTCAGCTACCTCTCATCCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCTTCTCGAACTGGAGATGCAGCTGGAGGAGCAGC
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA
AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAACTGGGCCGT
ACATGTGGATAAACCAGGAACTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT
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ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGACT
TGGTCCACGCTCCGTTACCCTTGACCTGGAAACGCTCGAGCCTGTGTGGTGAGGAGCAGGGGTCCCCC
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CCTGCCCTGGAACCTTTGGGCCTTTGTCCAAGCCCCGGCGGGAAGTGCAGCAGGACCCCGGGGATGA
TTGATGTCCGGAAAAACCCCTGTAAAGCCCTCGGGGCGAGCCCTGCCTTGAGGGGAGACTCCGAGCCT
GCTGAAAGGGGCAGCTGCCTGTTTTGCTTCTGTGAAGGGCAGTCCTTACCGCACACCCCTAAATCCAGG
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCCAAAGAAGTGGACCCTCATTT
AACAAAATAATATGCAAATTCACCACTTACTTCATGAAGCTGTGGTACCCAATTGCCGCCTTG
TCTTGCTCGAATCTCAGGACAATTCTGGTTTCAGGCGTAAATGGATGTGCTTGTAGTTACGGGGTTG
GCCAAGAATCATCACGAAAGGGTCGGTGGCAACCAGGTGTGGTTTAAATGGTCTTATGTATATAGG
GAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

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FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLELVRPGWGGLRLLNGLPPGSFVPRPHTAPLGGAHAHV
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPCLCLEELDAI PGSRVGGSKARVQARQVPPATAS
EWRLAQAAQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQKRRSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQORRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAAQSQQQIRGEIDS
LRQEKDSLLKQRLEIDGKLRQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

code	field	name	unit	code	field	name	unit
27	270000	270000	270000	27	270000	270000	270000
28	280000	280000	280000	28	280000	280000	280000
29	290000	290000	290000	29	290000	290000	290000
30	300000	300000	300000	30	300000	300000	300000
31	310000	310000	310000	31	310000	310000	310000
32	320000	320000	320000	32	320000	320000	320000
33	330000	330000	330000	33	330000	330000	330000
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40	400000	400000	400000	40	400000	400000	400000
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50	500000	500000	500000	50	500000	500000	500000
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66	660000	660000	660000	66	660000	660000	660000
67	670000	670000	670000	67	670000	670000	670000
68	680000	680000	680000	68	680000	680000	680000
69	690000	69					

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQLQCSKGTTDAPVGSGWLWCQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPIRSCTRNRHVLYP

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

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FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
AACCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG
GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCC
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTAGTGGTCCGCCCCACGCGGG
TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCCGCTGCTACCCCTG
CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTGGCGCGCGCTCCCCGCCCGCCC
GCCCCGCCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG
AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC
CCCGCAGGCGGAAGCCCTGGCCGCAGCCGCCAGGACGCGATTGGCCCCGGAACCTCGCGCCCCA
CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCT
GTGCACCGAGGAGGGGCCGCTGTGCGCGCAGCCCGAGTGCCCGAGGCTGCACCCGCGCTGCA
TCCACGTCGACACGAGCCAGTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTG
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACC
CTGTGTACGAGCCTGATCAGTGCTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC
AAATGTAGACGCTTCCCAGAACACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA
CATTCTAGATGACTCTGGGAACTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA
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TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL
GRPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTTPQAEALA
AAAQDAIGPELAPTPEPPPEEYVYPDYRGKGCVDSESGFVYAIGKFAKGPSACPCCLCTEEGPL
CAQPECPRLLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEETWR
IERQAMCTRHECRQM

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAAC
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CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTC
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GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAT
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GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
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CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTC
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCA
AACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRGGLIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSTNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG
GCTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTAGAGCCGAGGGACCCGGTGGC
CTCGTCGCTCAGCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT
TGTCGGGGCCCCGAGGCTCCGTGGCGGGACCCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG
CAGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT
GAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCG
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCGCTGCGGCTCATCACCAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCGCTTCTGCAGGGGCTGTGGCAGCACTACCACCCTGGC
TTGCCGCCCGCGGACGTCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT
GAGATTTTTTGTACTGTGAGAAGTTTTTAAGTGAAGTAGAAAAAATGCTACAGCTCTTT
ATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCT
ACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTTACCTG
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTACATAGATG
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTAT
ACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGC
AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA
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TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTCATAATAACACTTGAAAAGTGCT
GGAGTAACAAAATATCTCAGTTGGACCATCCTTAACTTGATTGAACTGTCTAGGAACTTTAC
AGATTGTTCTGCAGTTCTCTCTTTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC
AGGAATATTTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGAAAGTACAA
TGAAAATAAATATTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT
TTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTTCAATTCTGT
CACTTGGCTTCGATTTTTTATATTTTCTATTATATGAAATGTATCTTTTGGTTGTTTGATTT
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA
TAAAGAAAATTCTTGTGACTTTAAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSFYFGTKTRYEDVNPVLLS
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACCTGTCTTGCATCATTACGGATTTCGC
AGACAAGTGACCCAGGATCGAGTGAAGAAAATTCAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTTTCGCAATTCTTCTTTCCACTTAACTCTGAAACAGGCACTTTGGTGTTCCTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCAATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTTGGGGGGTTCTGGTTGTCTTGTCTGCTGACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTTACCCTGGTCTGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTATTTTATAAAATTT
TACATCTAAATTTTGTAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTCTTTCT
CACACAAGTTTTAGCCTTTTTCAAGGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGATG
CCAGTCAAGCTCCTGGGGTTGCGCCAGGCGCCCGCCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTAAGTTTGTTTAATTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT
CCCCTGTTCTCTTTGGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAAGCAGTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGGAGACACTGCTCCCAT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA
GAATGGCTCTCACTACTCACTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATACCTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCCGCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTATAGTGATAGGGTAGCCTTATGCCCCCTCTTCTTATACCTAAAACCTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTGTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCATTGTGTTAAC
CTCATTATATAAAGCTTCAAAAAACCCA

1000
900
800
700
600
500
400
300
200
100
0

[illegible]

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIGGIIGG
VLVVLAVLALITLGI CCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

cell	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
cell	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPPEEKPLPTAFLVDTSEEALLLPDWLKLRM
IRSEVLRLVDAALQDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRLQLCQYQRCVPQDTGFSSFLKVLLQMLQWLDSFG
VEGGPLRAQLRMLASQASAGRRLSDVRGGLLRLAELAEALAFRQDLEVVSSTVRAVIATLRSGEQ
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASPFPAACKPVVVVSSLLLQEEEP
GGKPGADGGSLEAVRLGPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQCIRVLLGKSREQRFDPSASLDFLWACIHPRIWQGRDQRTPOKR
REELVLRVQGPPELISLVELILAEAEATRSQDGDTAACSLIQARLPLLLSCCCGDDESVRKVTE
HLSGCIQQWGDSVLGRRCRDLLLQLYLQRPPELVPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMLIAALLHGRTHLNFQEFQONHL
SCFLHVLGLLELLQPHVFRSEHQGALWDCLLSFIRLLLNRYKSSRHAAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSIDIDMSRRRPEILSFFSTNLQRL
MSSAECCRNLAFLSLALRSMQNSPSIAAAFLPTFMYCLGSQDFEVVQTALRNLPYALLCQE
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

[illegible]

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLFFFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRLHAAEQESLKRSK
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVVRWRTKQNL
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPPFDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515